

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at line 21 of page 34 with the following paragraph:

As a method for screening for, for example, a protein (e.g., a ligand) binding to a protein of the present invention, many methods known by persons skilled in the art can be employed. Examples of such a screening method include immunoprecipitation (Harlow, E. and Lane, D.: Antibodies, pp. 511-552, Cold Spring Harbor Laboratory publications, New York (1988)), Western blotting method (Skolnik, E. Y. et al., Cell (1991) 65, 83-90), the 2-hybrid system using cells (Fields, S., and Sternglanz, R., Trend. Genet. (1994) 10, 286-292; and Dalton S, and Treisman R., (1992) Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element. Cell, 68, 597-612) ("MATCHMAKER Two-Hybrid System," "Mammalian ~~MATCHMAKER~~ MATCHMAKER[™] Two-Hybrid Assay Kit," "MATCHMAKER MATCHMAKER[™] One-Hybrid System." (all of them are produced by Clontech), and "~~HybriZAP~~ HYBRIZAP[™] Two-Hybrid Vector System" (produced by Stratagene)), a method utilizing affinity chromatography, and a method using a biosensor that utilizes the surface plasmon resonance phenomenon.

Please replace the paragraph beginning at line 12, page 41 with the following paragraph:

Next, *in vitro* transcription and translation (Promega, ~~TNT-T7~~ TNT T7™ Quick Coupled Transcription/Translation System cat.no.L1107) were carried out, and then clones for which products of 50 kDa or more had been confirmed were selected.

Please replace the paragraph beginning at line 16, page 41 with the following paragraph:

Next, the terminal nucleotide sequences of the selected clones were determined. With the thus obtained sequences as queries, the nr database (All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1, or 2 HTGS sequences)) was homology-searched using the BLASTN 2.2.1 homology search program (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," Nucleic Acids Res. 25: 3389-3402). For sequencing, a DNA sequencer (~~ABI PRISM377~~ ABI PRISM™ 377) produced by PE Applied Biosystem and a reaction kit produced by the same were used. Most sequences were determined by a dye terminator method using shotgun clones. Some nucleotide sequences were determined by synthesizing oligonucleotides based on the determined nucleotide sequences, and then carrying out a primer walking method.

Please replace the paragraph beginning at page 42, line 4, with the following paragraph:

By the use of an *in vitro* transcription and translation system (Promega, ~~TNT-T7~~ TNT T7[™] Quick Coupled Transcription/Translation System cat. no. L1107), a gene product from the cDNA clone FJ04470 was expressed.

Please replace the paragraph beginning at line 7, page 42, with the following paragraph:

The product, in which ³⁵S-labeled methionine had been incorporated was subjected to 12.5% SDS-PAGE electrophoresis. Gel was dried, autoradiography was carried out using a BAS2000 (FUJIFILM) system, and then the gene product of the clone FJ04470 was detected. The size of the FJ04470 product was 90 kDa as measured using a size marker (Cat. 161-0324) of Kaleidoseope KALEIDOSCOPE[™] Prestained Standards of Bio-Rad.

Please replace the paragraph beginning at line 13, page 47, with the following paragraph:

The amount of the transcript of the gene of the present invention was analyzed by the ~~ABI PRISM~~ ABI PRISM[™] (registered trademark) 7700 Sequence Detection System (ABI) using cDNAs of various tissues. For analysis of expression levels of GAPDH gene, a Pre-Developed ~~TaqMan~~ TAQMAN[™] PCR Assay Kit (ABI, #4310884E) was used. The composition for the PCR reaction was as follows. 5 µl of MTC Panel cDNA (Clontech) was added to Master Mix (a mixture of 1.25 µl of 20X Control Mix (GAPDH), 6.25 µl of DEPC-treated water (Ambion,

#9920), and 12.5 µl of ~~TaqMan~~ TAQMAN[™] Universal PCR Master Mix (ABI, #4304437)) to 25 µl. Gene amplification was carried out for 40 cycles, each cycle consisting of 50°C for 2 minutes, 95°C for 10 minutes, and 95°C for 15 seconds -60°C for 1 minute) using an ABI PRISM ABI PRISM[™] (registered trademark) 7700 Sequence Detection System of ABI on a MicroAmp Optical 96-Well Reaction Plate (ABI, #N801-0560). As MTC Panel cDNAs, Human MTC[™] Panel I (K1420-1), Human MTC[™] Panel II (K1421-1), and Human Tumor MTC[™] Panel I (K1422-1) of Clontech were used. Total RNA was collected by ISOGEN ISOGEN[™] (Wako Pure Chemical Industries) from the cultured carcinoma cells and then the genomic DNA was digested using amplification grade Dnase I (Invitrogen). The method was carried out according to the manual recommended by Invitrogen. The total RNA treated with DNase I was reverse-transcribed into a cDNA using Invitrogen superscript II reverse transcriptase.

Please replace the paragraph beginning at line 4, page 48, with the following paragraph:

Regarding the expression levels of the gene of the present invention, primer sequences that were optimal for RT-PCR were searched for using PrimerExpress 1.5 of ABI. When the sequence of the FJ04470 gene was compared with the genome sequence, the sequence matched the sequence of AC016168.18. As a result of analyzing intron and exon structures, the presence of an intron comprising approximately 2260 nucleotides were inferred in the vicinity of the nucleotide number of 2158 of FJ04470. Thus, primer positions were determined so that they sandwiched the region. When primer 4470-2043 (5'-AGATCCATGGCACC GTGTACTAC-3') and primer 4470-2230 (5'-GAAGATGCAACCATTGGCG-3') are used, 188 nucleotides will be

amplified in the case of cDNA and approximately 2450 nucleotides will be amplified in the case of the genome. 0.5 μ l of 10 μ M primer 4470-2043, 0.5 μ l of 10 μ M primer 4470-2230, 6.5 μ l of DEPC-treated water, and 12.5 μ l of SYBR Green PCR Master Mix (ABI, #4309155) were mixed to 20 μ l. 1 μ l of MTC Panel cDNA (Clontech) and 4 μ l of DEPC-treated water (treated water) were added to the mixed solution to 25 μ l. Gene amplification was carried out for 40 cycles, each cycle consisting of 50°C for 2 minutes, 95°C for 10 minutes, and 95°C for 20 seconds-60°C for 1 minute) using an ~~ABI-PRISM~~ ABI PRISM[™] (registered trademark) 7700 Sequence Detection System of ABI on the MicroAmp Optical 96-Well Reaction Plate of ABI (ABI, #N801-0560). A standard curve was created using a plasmid into which a GAPDH amplicon (the expression level of the GAPDH gene was used as an internal control) had been cloned. Based on the curve, the number of copies existing in the reaction solution was calculated. Table 3 below shows the results of comparing the expression levels in different tissues using relative values obtained by dividing each expression level of the gene of the present invention by each expression level of the GAPDH gene.